This week in techniques

Approach	Summary	Licensing status	Publication and contact information
Drug platforms			
Crystal structures of sirtuin 1 (SIRT1), SIRT2 and SIRT3 bound to inhibitors	<p>Crystal structures of sirtuins bound to inhibitors could guide the development of compounds directed against specific sirtuins. Crystal structures of a SIRT1 inhibitor bound to SIRT1, SIRT3 or a bacterial Sirt2 showed the compound co-occupied a conserved pocket alongside the enzyme's catalytic product, thereby preventing product release. The co-crystal structures also showed no structural differences between the conserved pockets of the three sirtuins that could account for their differing binding affinities for the inhibitor. Crystal structures of a SIRT3 inhibitor bound to SIRT3 showed the compound simultaneously occupied the acetyllysine binding site and the conserved pocket. Ongoing work includes using the structural data to develop specific inhibitors of SIRT3.</p> <p>SciBX 6(31); doi:10.1038/scibx.2013.841 Published online Aug. 15, 2013</p>	Unpatented; unlicensed; available for partnering	<p>Gertz, M. <i>et al. Proc. Natl. Acad. Sci. USA</i>; published online July 9, 2013; doi:10.1073/pnas.1303628110</p> <p>Nguyen, G.T.T. <i>et al. Acta Crystallogr. D. Biol. Crystallogr.</i>; published online July 17, 2013; doi:10.1107/S0907444913015448</p> <p>Contact: Clemens Steegborn, University of Bayreuth, Bayreuth, Germany e-mail: clemens.steegborn@uni-bayreuth.de</p>